

OS79Y4\_HUMAN  
ID OS79Y4\_HUMAN PRELIMINARY; PRT; 317 AA.  
AC OS79Y4;  
DT 01-FEB-2005 (Tremblrel. 29, Created)  
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)  
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)  
DR Tumor necrosis factor (ligand) superfamily, member 11 (Fragment).  
GN Name=TNFSP11; OSNames=RP11-86N24.2-001;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Pelan S.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL139382; CA16926.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
FT NON TER 317  
SQ SEQUENCE 317 AA; 35478 MW; 76617646348097P CRC64;  
Query Match 100.0%; Score 1685; DB 2; Length 317;  
Best Local Similarity 100.0%; Pred. No. 6.5e-136;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRASRDYTKYLRGSEEMGGGAPGAPHEGPAHPAPPAPAPAPASRSMFVALLGLGLGV 60  
DB 1 MRASRDYTKYLRGSEEMGGGAPGAPHEGPAHPAPPAPAPAPASRSMFVALLGLGLGV 60  
QY 61 VCSVALFFYPRAQNDPNRISDGTCTIRIIRHENDPOTTLSSQDTKLIIPSCRRIX 120  
DB 61 VCSVALFFYPRAQNDPNRISDGTCTIRIIRHENDPOTTLSSQDTKLIIPSCRRIX 120  
QY 121 QAFQAGAVQKELQHTVGSQHTPAEKAMVDGSLDLAKSKLEAOPFAHLLTNATDIPSGSH 180  
DB 121 QAFQAGAVQKELQHTVGSQHTPAEKAMVDGSLDLAKSKLEAOPFAHLLTNATDIPSGSH 180  
QY 181 KVLSSWYHNRGMAKISNMTFSPNGKLIIVDGFYLLANICFRHETSGDLATEYLQLMV 240  
DB 181 KVLSSWYHNRGMAKISNMTFSPNGKLIIVDGFYLLANICFRHETSGDLATEYLQLMV 240  
QY 241 YVTKTSIKIPSSHTLKKSGSTKXSGSEFHFPSINVGFPFKLRSGEISIEVSNPSILD 300  
DB 241 YVTKTSIKIPSSHTLKKSGSTKXSGSEFHFPSINVGFPFKLRSGEISIEVSNPSILD 300  
QY 301 PQQDATYFGAFKVRDID 317  
DB 301 PQQDATYFGAFKVRDID 317

## RESULT 3

TNFI\_MOUSE  
ID TNFI\_MOUSE STANDARD; PRT; 316 AA.  
AC OS3235; OS3506; OSJUK8; OSJUK9; OSR110;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-differentiation factor) (TRANCE) (osteoprotegerin ligand) (OPGL) (osteoclast superfamily member 11, membrane form; Tumor necrosis factor ligand superfamily member 11, soluble form).  
GN Name=tnfrsf11; Synonyms=Op91, Rankl, Trance;  
OS Mus musculus (mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC TISSUE=Hybridoma;  
RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;  
RA Wong B.R., Rno J., Arion J., Robinson E., Orlicki J., Chao M.,  
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
RA Choi Y.;  
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates C-Jun N-terminal kinase in T cells.";  
RL J. Biol. Chem. 272:25190-25194(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC TISSUE=Thymic Lymphoma;  
RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougan W.C.,  
RA Tomersko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,  
RA Gallibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";  
RL Nature 390:175-179(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC TISSUE=Bone marrow;  
RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;  
RA Lacey D.L., Timme E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Ri A., Qian Y.-X.,  
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
RA Boyle W.J.;  
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";  
RL Cell 93:165-176(1998).  
RN [4]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC TISSUE=Bone marrow stroma;  
RX MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;  
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,  
RA Mochizuki S.-I., Tomiyasu A., Yano K., Goto M., Murakami A., Tada E.,  
RA Motomura T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
RT "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
RN [5]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC STRAIN=129;  
RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;  
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
RA Ueda M., Higashio K.;  
RT "Cloning and characterization of the gene encoding mouse osteoclast differentiation factor.";  
RL Gene 230:121-127(1999).  
RN [6]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;  
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;  
RT "Determination of three isoforms of the receptor activator of nuclear factor-kappaB ligand and their differential expression in bone and thymus.";  
RL Endocrinology 142:1419-1426(2001).  
RN [7]  
RP PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION  
RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;  
RA Lum L., Wong B.R., Josien R., Becherer J.D., Edjument-Bromage H.,  
RA Schleindorff J., Tempst P., Choi Y., Blobel C.P.;  
RT "Evidence for a role of a tumor necrosis factor- $\alpha$ 1pha (TNF- $\alpha$ 1pha) -member involved in osteoclastogenesis and dendritic cell survival.";  
RL J. Biol. Chem. 274:13613-13618(1999).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
RX Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;  
RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants

RT of receptor-ligand specificity." ;  
 RT Clin. Invest. 108:971-979 (2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-216.  
 RX MEDLINE-21839021; PubMed-11733492; DOI=10.1074/jbc.M106225200;  
 RA Ito S., Wakabayashi K., Uekata O., Hayashi S., Okada F., Hata T.;  
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at  
 2.2-A resolution." ;  
 RL J. Biol. Chem. 277:6631-6636 (2002).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hyperalgesia of malignancy.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted  
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O35235-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O35235-2; Sequence=VSP\_006449;  
 CC Name=3;  
 CC IsoId=O35235-3; Sequence=VSP\_006448;  
 CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,  
 CC but not in nonlymphoid tissues and is abundantly expressed in T  
 CC cells but not in B cells. A high level expression is also seen in  
 CC the trabecular bone and lung.  
 CC -1- PTM: N-glycosylated.  
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing. The cleavage may be catalyzed by  
 CC ADAM17. A further shorter soluble form was observed.  
 CC -1- DISEASE: Deficiency in Tnfrsf11 results in failure to form lobulo-  
 CC alveolar mammary structures during pregnancy, resulting in death  
 CC of newborns. Transc-deficient mice show severe osteopetrosis, with  
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit  
 CC profound growth retardation at several skeletal sites, including  
 CC the limbs, skull, and vertebrae and have marked chondrodysplasia,  
 CC with thick, irregular growth plates and a relative increase in  
 CC hypertrophic chondrocytes.  
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: AF013170; AAC71061.1; -; mRNA.  
 CC EMBL: AF019048; AAB6812.1; -; mRNA.  
 CC EMBL: AF053713; AAC40113.1; -; mRNA.  
 CC EMBL: AB008426; BAA25425.1; -; mRNA.  
 CC EMBL: AB022039; BAA36970.1; -; Genomic DNA.  
 CC EMBL: AB032771; BAA97257.1; -; mRNA.  
 CC EMBL: AB032772; BAA97258.1; -; mRNA.  
 CC EMBL: AB036798; BAA97259.1; -; mRNA.  
 CC PDB: 1IOA; X-ray; A/B/C=157-316.  
 CC PDB: 1J7Z; X-ray; X/Y/Z=156-316.  
 CC EMBL: ENSMUSG0000022015; Mus musculus.  
 CC PDB: MGI:1100089; Tnfrsf11.  
 CC DR MGI: GO:0016021; C: integral to membrane; TNF.  
 CC DR GO: GO:0005515; P: protein binding; IPI.  
 CC DR GO: GO:0045453; P: bone resorption; IDA.  
 CC DR GO: GO:0007515; P: lymph gland development; IDA.  
 CC DR GO: GO:0009887; P: organogenesis; IMP.  
 CC DR GO: GO:0001503; P: ossification; IMP.  
 CC DR GO: GO:0045672; P: positive regulation of osteoclast different. . . IDA.  
 CC DR GO: GO:0051260; P: protein homooligomerization; IDA.  
 CC DR InterPro: IPR006052; TNF\_family.

DR InterPro: IPR003636; TNF\_subf.  
 DR Pfam: PF00229; TNF\_1.  
 DR ProDom: PD002012; TNF\_subf; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 DR 3D-structure; Alternative splicing; Cytokine; Developmental protein;  
 KW Differentiation; Direct protein sequencing; Glycoprotein; Receptor;  
 KW Signal-anchor; Transmembrane.  
 FT CHAIN 1 316  
 FT FT  
 FT CHAIN 139 316  
 FT FT  
 FT TOPO\_DOM 1 48  
 FT FT  
 FT TRANSMEM 49 69  
 FT FT  
 FT TOPO\_DOM 70 316  
 FT FT  
 FT SITE 138 139  
 FT FT  
 FT CARBOHYD 197 197  
 FT FT  
 FT CARBOHYD 262 262  
 FT FT  
 FT VARSPLIC 1 117  
 FT FT  
 FT VARSPLIC 14 44  
 FT FT  
 FT SSEEKSGGVPEHGPPLHPAPAPAPAPPA -> TP (in  
 FT isoform 2).  
 FT FTId=VSP\_006449.  
 FT G -> D (in Ref. 2).  
 FT Missing (in Ref. 5).  
 FT  
 FT CONFLICT 99 99  
 FT FT  
 FT CONFLICT 141 143  
 FT FT  
 FT STRAND 164 169  
 FT FT  
 FT TURN 171 172  
 FT FT  
 FT STRAND 181 182  
 FT FT  
 FT STRAND 186 187  
 FT FT  
 FT TURN 191 192  
 FT FT  
 FT STRAND 194 196  
 FT FT  
 FT STRAND 198 201  
 FT FT  
 FT TURN 202 203  
 FT FT  
 FT STRAND 204 207

Query Match 84.1%; Score 1417.5; DB 1; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 5.7e-113;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
 QY 1 MRASRYTKTLRSGEMGGPGAPHEGPIH-APPAPHPAPAPASRMFVALGLGIGQ 59  
 DB 1 MRASRDYGYKLNSSEMGSGPVHEGPPLHPAPAPAPAPAPASRMFLALGLGIGQ 60  
 QY 60 VCSVALFFYFRQMDNRISEDDTHCTIYILRLHENAADQDTTLESQDTKLIPDSGRRI 119  
 DB 61 VCSIALFLYFRQMDNRISEDDTHCTIYILRLHENAAGLQDSTLESQDT--LPDSGRRI 118  
 QY 120 KQAFQAVQKELOHIVGSOHIBAEKAMVDGSMWDLAKRSLEAEOPPHLITNATIDPSGS 179  
 DB 119 KQAFQAVQKELOHIVGPOKPSGAPPMESGSLDVQKRGKPEAPPAHLITINASIPSGS 178  
 QY 180 HKYSLSSWTHDRGMWAKISNMTFNGKLIYNQDGYLLYANICFRHHTSGDLATEYLQIM 239  
 DB 179 HKYTLSSWTHDRGMWAKISNMTLSNGKLRVNDGFYLLYANICFRHHTSGSVTDVLQIM 238  
 QY 240 VYVTKTSIKIPSSHTLMKSGSTYVNGSBEFHYYSINVGAFPKLRSGBEISIVSNPSLL 299  
 DB 239 VYVTKTSIKIPSSHNLMKSGSTKWSGNSBEFHYYSINVGAFPKLRAGEISIVSNPSLL 298  
 QY 300 DPQDQATYFGAFKVDID 317  
 DB 299 DPQDQATYFGAFKVDID 316

RESULT 4  
 ID TNF11 RAT STANDARD; PRT; 318 AA.  
 AC Q9ESB2; Q91Z19;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

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FT      TURN      202      203
FT      STRAND    204      207

Query Match      100.0%; Score 148; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAASIPSGSHKVTLSWYHDSGMAKIS 27
DB      170 NAASIPSGSHKVTLSWYHDSGMAKIS 196

RESULT 2
ID      TNF1L_RAT      STANDARD;      PRT;      318 AA.
AC      Q9SESE2; Q91219;
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE      of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE      induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE      differentiation factor) (ODF) [contains: Tumor necrosis factor ligand
DE      superfamily member 11, membrane form; Tumor necrosis factor ligand
DE      superfamily member 11, soluble form].
GN      Name=TNF11; Synonym=Op1, Rankl, Trance;
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      TISSUE=Tibial bone;
RX      MEDLINE=20540945; PubMed=11092398;
RA      Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA      Zheng M.H.;
RT      "Cloning, sequence and functional characterization of the rat
RT      homologue of receptor activator of NF-kB ligand.";
RL      J. Bone Miner. Res. 15:2178-2186(2000).
[2]
RN      NUCLEOTIDE SEQUENCE OF 266-318.
RC      STRAIN=Fischer 344;
RX      MEDLINE=21662371; PubMed=11804028;
RA      Odegren P.R., Kim N., van Weesebeek L., Mackay C., Mason-Savas A.,
RA      Safadi F.P., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA      Marks S.C. Jr.;
RT      "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT      the TNFRSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
RL      Int. J. Dev. Biol. 45:853-859(2001).
[1]
RN      FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
RN      TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
RN      Augments the ability of dendritic cells to stimulate naive T-cell
RN      proliferation. May be an important regulator of interactions
RN      between T cells and dendritic cells and may play a role in the
RN      regulation of the T cell-dependent immune response. May also play
RN      an important role in enhanced bone resorption in humoral
RN      hypercalcemia of malignancy.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC      similarity).
CC      -1- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC      -1- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -1- SIMILARITY: Belongs to the tumor necrosis factor family.

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removed.

EMBL, AF187319; ABG17031.1; -, mRNA.

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DR      EMBL; AF425669; AAL23963.1; -, mRNA.
DR      HSSP; O35235; 1J7Z.
DR      SMR; Q9SESE2; 163-318.
DR      Ensembl; ENSRNOG0000009559; Rattus norvegicus.
DR      RGD; 620784; Tnfef11.
DR      GO; GO:0045780; P:positive regulation of bone resorption; IMP.
DR      GO; GO:0045672; P:positive regulation of osteoclast different. . .; IMP.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      PROSITE; PS00049; TNF_2; 1.
KW      Cytokine; Developmental protein; Differentiation; Glycoprotein;
KW      Receptor; Signal-anchor; Transmembrane.
FT      CHAIN      1      318
FT
FT      CHAIN      141      318
FT
FT      TOPO_DOM      1      47
FT      TRANSMEM      48      68
FT
FT      TOPO_DOM      69      318
FT      SITE      140      141
FT      CARBOHYD      199
FT      CARBOHYD      264
FT      CONFLICT      317
FT      SEQUENCE      318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match      94.6%; Score 140; DB 1; Length 318;
Best Local Similarity 92.6%; Pred. No. 2.8e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAASIPSGSHKVTLSWYHDSGMAKIS 27
DB      172 NAADIPSGSHKVTLSWYHDSGMAKIS 198

RESULT 3
ID      O54A98 HUMAN
AC      O54A98;
DT      13-SEP-2005 (TrEMBLrel. 31, Created)
DT      13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE      Receptor activator of nuclear factor kappa B ligand 3.
GN      Name=hRANKL 3;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC      Homo.
OX      NCBI_TaxID=9606;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      PubMed=14751335; DOI=10.1016/j.jbrc.2003.12.191;
RA      Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai M., Utsuyama M.,
RA      Tatsumi M., Dematsu H., Hirokawa K.;
RT      "Regulation of osteoclastogenesis by three human RANKL isoforms
RT      expressed in NIH3T3 cells.";
RL      Biochem. Biophys. Res. Commun. 314:1021-1027(2004).
DR      EMBL; AB064268; BAB79693.1; -, mRNA.
KW      Receptor.
SQ      SEQUENCE      244 AA; 27690 MW; C8275906848B83C CRC64;

Query Match      91.9%; Score 136; DB 2; Length 244;
Best Local Similarity 88.9%; Pred. No. 7.8e-11;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NAASIPSGSHKVTLSWYHDSGMAKIS 27
DB      98 NAADIPSGSHKVTLSWYHDSGMAKIS 124

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FT TURAN 202 203  
FT STRAND 204 207

Query Match 100.0%; Score 84; DB 1; Length 316;  
Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYVVKTSIKIPSSHNL 17  
DB 239 VYVVKTSIKIPSSHNL 255

RESULT 2  
ID TNF11 RAT STANDARD; PRT; 318 AA.

AC Q9SEB2; Q91Z19;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 11 (receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand superfamily member 11, membrane form; Tumor necrosis factor ligand superfamily member 11, soluble form].  
GN Name=TNF11; Synonyms=Oppl, Rankl, Trance;  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN 11  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE= tibial bone;  
RX MEDLINE=20540945; PubMed=11092398;  
RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S., Zheng M.H.;  
RT Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand.;  
RL J. Bone Miner. Res. 15:2178-2186(2000).  
RN 12  
RP NUCLEOTIDE SEQUENCE OF 266-318.  
RC STRAIN= Fischer 344;  
RX MEDLINE=21662371; PubMed=11804028;  
RA Osdoren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savars A., Safadi F.P., Popoff S.N., Lengner C., van-Hul W., Choi Y., Marks S.C. Jr.;  
RT Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TNFRSF11 (TRANCE, RANKL, ODF, OPGL) gene.;  
RL Int. J. Dev. Biol. 45:853-859(2001).  
CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcaemia of malignancy.  
CC -1- SUBUNIT: Homotrimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).  
CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.  
CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).  
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.  
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CC EMBL, AF187319; AAG17031.1; -, mRNA.

DR EMBL; AF425669; AAL23963.1; -, mRNA.  
DR HSSP; O35235; 1J72.  
DR SMR; Q9SEB2; 163-318.  
DR Ensembl; ENSRNOG0000009559; Rattus norvegicus.  
DR RGD; 620784; Tnfrsf11.  
DR GO; GO:0045780; P:positive regulation of bone resorption; IMP.  
DR GO; GO:0045672; P:positive regulation of osteoclast different. . .; IMP.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
DR PROSITE; PS50049; TNF\_2; 1.  
KW Cytokine; Developmental protein; Differentiation; Glycoprotein; Receptor; Signal-anchor; Transmembrane.  
FT CHAIN 1 318  
FT CHAIN 141 318  
FT TOPO\_DOM 1 47  
FT TRANSMEM 48 68  
FT FT  
FT TOPO\_DOM 69 318  
FT SITE 140 141  
FT CARBOHYD 199 199  
FT CARBOHYD 264 264  
FT CONFLICT 317 317  
SQ SEQUENCE 318 AA; 35370 MW; 4B87AD706AD098F CRC64;

Query Match 100.0%; Score 84; DB 1; Length 318;  
Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYVVKTSIKIPSSHNL 17  
DB 241 VYVVKTSIKIPSSHNL 257

RESULT 3  
ID 054A98 HUMAN PRELIMINARY; PRT; 244 AA.  
AC 054A98;  
DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)  
DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)  
DE Receptor activator of nuclear factor kappa B ligand 3.  
GN Name=hRANKL 3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; OC Homo.  
OX NCBI\_TaxID=9606;  
RN 11  
RP NUCLEOTIDE SEQUENCE.  
RC PubMed=14751235; DOI=10.1016/j.bbr.2003.12.191;  
RX Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai M., Utsuyama M., Tatematsu M., Uematsu H., Hirokawa K.;  
RT Regulation of osteoclastogenesis by three human RANKL isoforms expressed in NIH3T3 cells.;  
RL Biochem. Biophys. Res. Commun. 314:1021-1027(2004).  
DR EMBL; AB064268; BAB79693.1; -, mRNA.  
KW Receptor.  
SQ SEQUENCE 244 AA; 27690 MW; C827590684B6B83C CRC64;

Query Match 88.1%; Score 74; DB 2; Length 244;  
Best Local Similarity 88.2%; Pred. No. 0.00015;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VYVVKTSIKIPSSHNL 17  
DB 167 VYVVKTSIKIPSSHNL 183